P6.03 - Exploiting genetic resources for developing rice germplasm with eco-efficient water use

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The Cirad/CIAT rice collaborative project focuses on the development and enhancement of rice composite populations (CPs) through recurrent selection (RS) breeding. Our goal is to develop and diffuse improved material for various rainfed ecosystems in Latin America and the Caribbean (LAC). Our breeding strategy is based on the development of broad-base populations; their improvement thought RS and the exploitation of their genetic wealth for line development.
From a base population, four CP were derived, some subjected to selections under acid soils conditions (savannas of Colombian Llanos), others selected under the conditions of Bolivian rice agriculture. We used 16 SSR loci to assess the genetic diversity within these populations and estimate genetic differentiation between them. We applied large scale phenotyping method adapted to field conditions to evaluate the response to drought. Through thermographic infra-red technology (IR) we screened S_1 progenies extracted from each population which were exposed to a 15-day drought period at flowering stage.
Allelic variability measured in the four CP revealed high levels of neutral diversity. The genetic diversity expressed in terms of number of observed alleles per locus (*Na*) and Shannon diversity index (*I*), was high within the populations (*Na* > 3.133, and *I* = 0.693 to *I* = 0.800). Significant allelic and genotypic differentiations were found at most loci. A total of six alleles were found with frequency > 5% and unique to a particular population. IR screening showed that the CPs hold favorable alleles for resilience to drought. S_1 lines with cool canopy temperatures during the dry period indicated good capacity to maintain transpiration and thus sustained growth under water stress conditions. These lines are potential progenitors to develop a new population with increased eco-efficiency to water use.
Besides showing the genetic wealth retained in these CP, our work presents an advance towards the integration of high-throughput phenotyping and use of molecular markers for improving RS breeding strategy. Our objective is not limited to integrating disciplines; the outcomes of the project, both methodologies and germplasm, are shared among our network of rice breeders from LAC.